

GenCore version 5.1.4.D5.4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:46:23 ; Search time 43.7273 Seconds

(without alignments)
1225.145 Million cell updates/sec

Title: US-09-988-971-2_COPY_2_261

Perfect score: 1346
Sequence: 1 GSLPGRKSLSPSPSSSVQ.....RESLSPYSLNDEAVSDDA 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum March 0%

Maximum March 100%
Listing first 45 summaries

Database :

1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP_mmc: *
8: SP_organelle: *
9: SP_plant: *
10: SP_rhiz: *
11: SP rodent: *
12: SP virus: *
13: SP_vertebrate: *
14: SP_unclassified: *
15: SP_virus: *
16: SP_bacteriophage: *
17: SP_archaeal: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1346	100.0	261	4 Q9H6Q3	Q9H6Q3 homo sapien
2	1040	77.3	197	4 Q9H135	Q9H135 homo sapien
3	1027	76.3	259	11 Q8V142	Q8V142 mus musculu
4	1018	75.6	259	11 Q8V140	Q8V140 mus musculu
5	933.5	69.4	179	4 Q8WY18	Q8WY18 homo sapien
6	751.5	55.8	179	11 Q8WY18	Q8WY18 mus musculu
7	495.5	36.8	280	11 Q8QZK8	Q8QZK8 mus musculu
8	495.5	36.8	281	11 Q8QZK8	Q8QZK8 mus musculu
9	485.5	36.1	276	4 Q13339	Q13339 homo sapien
10	370.5	27.5	502	13 Q9DDK6	Q9DDK6 salmo salar
11	364.5	27.1	488	13 Q13064	Q13064 xenopus lae
12	362.5	26.9	161	4 Q9H17	Q9H17 homo sapien
13	356.5	26.5	505	4 Q9H17	Q9H17 homo sapien
14	344	25.6	509	6 Q9SM32	Q9SM32 hyllobates s
15	342.5	25.4	509	11 Q91X65	Q91X65 mus musculu
16	336	25.0	517	5 Q9V9J3	Q9V9J3 drosophila

17	332	24.7	509	6 Q95KX7	Q95KX7 salmtr sci
18	319.5	22.7	537	11 Q62844	Q62844 rattus norv
19	315	23.4	496	13 Q93411	Q93411 xenopus lae
20	313.5	23.3	541	11 Q99PW1	Q99PW1 rattus norv
21	313	23.3	812	15 Q85466	Q85466 y73 barcoma
22	311	23.1	517	11 Q63206	Q63206 rattus norv
23	310	23.0	534	4 Q16248	Q16248 homo sapien
24	310	23.0	534	6 Q95M31	Q95M31 hyllobates s
25	309	23.0	527	5 Q9Y121	Q9Y121 ephydaria f
26	307.5	22.8	517	5 Q77050	Q77050 anthocidari
27	301	22.4	63	4 Q96Q14	Q96Q14 homo sapien
28	292.5	21.7	587	15 Q64817	Q64817 avian sarco
29	289	21.5	511	5 Q8WQMS	Q8WQMS strongyloce
30	288.5	21.4	503	5 Q8WSU5	Q8WSU5 ephydaria f
31	286	21.2	502	13 Q8Q3J9	Q8Q3J9 fuqu rubrip
32	284.5	21.1	523	15 Q85477	Q85477 rous sarcom
33	284.5	21.1	526	15 Q64994	Q64994 rous sarcom
34	281.5	20.9	526	15 Q93080	Q93080 rous sarcom
35	280	20.8	535	15 Q92957	Q92957 rous sarcom
36	279.5	20.8	526	15 Q64993	Q64993 rous sarcom
37	279	20.7	546	15 Q86363	Q86363 rous sarcom
38	277.5	20.6	526	15 Q92806	Q92806 rous sarcom
39	277.5	20.6	542	11 Q9UJ10	Q9UJ10 rattus norv
40	277	20.6	545	15 Q86362	Q86362 rous sarcom
41	274.5	20.4	495	5 Q8WSU4	Q8WSU4 ephydaria f
42	274	20.4	504	5 Q8WSU2	Q8WSU2 ephydaria f
43	273.5	20.3	526	15 Q07461	Q07461 rous sarcom
44	272.5	20.2	526	15 Q60567	Q60567 rous sarcom
45	264.5	19.7	507	5 Q45539	Q45539 caenorhabdi

ALIGNMENTS

RESULT 1

Q9H6Q3 PRELIMINARY; PRT; 261 AA.

AC Q9H6Q3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CDNA: FL219922 fls, clone HEP0554 (Src-like adapter protein-2)
DE (Modulator of antigen receptor signaling MARS).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hiki T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani T., Oka T., Suzuki Y., Obayashi M., Niemi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.,
RT "NEDO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21553259; PubMed=11696592;
RA Holland S.O., Liao X.C., Mendemali M.K., Zhou X., Pardo J., Chu P.,
RA Spencer C., Fu A.C., Sheng N., Yu P., Pail E., Nagin A., Shen M.,
RA Yu S., Chan E., Wu X., Li C., Woloszewski M., Aversa G.,
RA Kolbinger F., Bennett M.K., Moliniaux S., Luo Y., Payan D.G.,
RA Mancoff H.S.V., Wu J.,
RT "Functional cloning of Src-like adapter Protein-2 (SLAP-2), a Novel
RT Inhibitor of Antigen Receptor Signaling."
RL J. Exp. Med. 194:1263-1276(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Loreto M.P., McGlade C.J.,
RT "Modulator of Antigen Receptor Signaling (MARS)."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; AK025645; BAB15201.1; -.

DR EMBL; AF36353; AAL29204.1; -
 DR EMBL; AF290985; AAL38197.1; -
 DR HSSP; P06239; LK.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KM SH3 domain; Receptor
 SQ SEQUENCE 261 AA; 28585 MW; 858AF03451672B3D CRC64;

Query Match 100.0%; Score 1346; DB 4; Length 261;
 Best Local Similarity 100.0%; Pred. No. 4,9e-115;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSLSRRKSLSPSSSSVGGGPTVMEERSKATVALGSPAGPAELSLRLGEP LTI 60
 DB 2 GSLSRRKSLSPSSSSVGGGPTVMEERSKATVALGSPAGPAELSLRLGEP LTI 61
 QY 61 VSEDDDMWTVLSEVSGREYNIPSVHAKVSHGWLVEGLSREKAEELLPLPGNGCAF LIR 120
 DB 62 VSEDDDMWTVLSEVSGREYNIPSVHAKVSHGWLVEGLSREKAEELLPLPGNGCAF LIR 121
 QY 121 ESQTRRGYSYLSVRLSRPASWDRIRHRIHCLDNGMLYSRLTFFPSLQALVDHYSELAD 180
 DB 122 ESQTRRGYSYLSVRLSRPASWDRIRHRIHCLDNGMLYSRLTFFPSLQALVDHYSELAD 181
 QY 181 DICLLKEPCVLQAGPLPGKDIPLPVTVOPTPLNWKELDSLLFSEATGSESLSEGL 240
 DB 182 DICLLKEPCVLQAGPLPGKDIPLPVTVOPTPLNWKELDSLLFSEATGSESLSEGL 241
 QY 241 REELSIFYISLNDENVSLDDA 260
 DB 242 REELSIFYISLNDENVSLDDA 261

RESULT 2
 Q9H135 PRELIMINARY; PRT; 197 AA.

ID Q9H135
 AC Q9H135;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE D9J77B1.1 (Novel protein tyrosine kinase with Src homology domain 2 (SH2) domain) (Fragment).
 GN D9J77B1.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]_TaxId=9606;
 RP SEQUENCE FROM N.A.
 RA LLOYD D.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL050318; CAB75365.1; -
 DR HSSP; P06239; LK.
 DR InterPro; IPR000980; SH2.
 DR Pfam; PF00017; SH2; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PS50001; SH2; 1.
 KM Kinase.
 FT NON TER
 SQ SEQUENCE 197 AA; 22124 MW; EF01FE7A85C5C1F1 CRC64;

Query Match 77.3%; Score 1040; DB 4; Length 197;
 Best Local Similarity 100.0%; Pred. No. 3.3e-87;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 64 DGDWMTVLSVSGREYNIPSVHAKVSHGWLVEGLSREKAEELLPLPGNGCAF LIR ESQ 123
 DB 1 DGDWMTVLSVSGREYNIPSVHAKVSHGWLVEGLSREKAEELLPLPGNGCAF LIR ESQ 120
 QY 124 TRRGYSYLSVRLSRPASWDRIRHRIHCLDNGMLYSRLTFFPSLQALVDHYSELADIC 183
 DB 61 TRRGYSYLSVRLSRPASWDRIRHRIHCLDNGMLYSRLTFFPSLQALVDHYSELADIC 120
 QY 184 CLKEPCVLQAGPLPGKDIPLPVTVOPTPLNWKELDSLLFSEATGSESLSEGLRES 243
 DB 121 CLKEPCVLQAGPLPGKDIPLPVTVOPTPLNWKELDSLLFSEATGSESLSEGLRES 180
 QY 244 LSIFYISLNDENVSLDDA 260
 DB 181 LSIFYISLNDENVSLDDA 197

RESULT 3

OSV142 PRELIMINARY; PRT; 259 AA.
 ID OSV142
 AC OSV142;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-UN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Modulator of antigen receptor signaling MARS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Loreto M.P.; McGlade C.J.;
 RT "Modulator of Antigen Receptor Signaling (MARS)".
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF287467; AAL38196.1; -
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KM Receptor.
 SQ SEQUENCE 259 AA; 28476 MW; 8270F17CD3F50A3 CRC64;

Query Match 76.3%; Score 1027; DB 11; Length 259;
 Best Local Similarity 79.7%; Pred. No. 7.4e-86;
 Matches 208; Conservative 16; Mismatches 33; Indels 4; Gaps 3;

QY 1 GSLSRRKSLSPSSSSVGGGPTVMEERSKATVALGSPAGPAELSLRLGEP LTI 60
 DB 2 GSLSRRKSLSPSSSSVGGGPTVMEERSKATVALGSPAGPAELSLRLGEP LTI 60
 QY 61 VSEDDDMWTVLSEVSGREYNIPSVHAKVSHGWLVEGLSREKAEELLPLPGNGCAF LIR 120
 DB 61 VSEDDDMWTVLSEVSGREYNIPSVHAKVSHGWLVEGLSREKAEELLPLPGNGCAF LIR 120
 QY 121 ESQTRRGYSYLSVRLSRPASWDRIRHRIHCLDNGMLYSRLTFFPSLQALVDHYSELAD 180
 DB 121 ESQTRRGYSYLSVRLSRPASWDRIRHRIHCLDNGMLYSRLTFFPSLQALVDHYSELAD 180
 QY 181 DICLLKEPCVLQAGPLPGKDIPLPVTVOPTPLNWKELDSLLFSEATGSESLSEGL 239
 DB 181 GICCLKEPCVLQAGPLPGKDIPLPVTVOPTPLNWKELDSLLFSEATGSESLSEGL 240
 QY 240 LRELSIFYISLNDENVSLDDA 260

DB 241. LRESLSYSISLAED--PLDDA 259

RESULT 4

ID Q08410 PRELIMINARY; PRT; 259 AA.

AC Q08410; 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

OS Src-like adapter protein-2.

OC Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OK NCBI_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Pandey A., Ibarrola N., Kratchmarova I., Fernandez M.,

RA Constantinescu S., Onara O., Sawadiksol S., Lodish H.F., Mann M.,

RT "A novel Src homology 2 domain-containing molecule, Src-Like Adapter

RT Protein-2 (SLAP-2), which negatively regulates T cell receptor

RL signaling."

RN Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.

RP SEQUENCE FROM N.A.

RA Ibarrola N., Mann M., Pandey A.

RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF434990; AAL6403.1; -

SQ SEQUENCE 259 AA; 28516 MW; 138868244152834 CRC64;

Query Match 75.6%; Score 1018; DB 11; Length 259;

Best Local Similarity 79.3%; Pred. No. 4.9e-85;

Matches 207; Conservative 16; Mismatches 34; Indels 4; Gaps 3;

QY 1 GSLPSRRKSLPSPLSSVQGGPYTMEARSKATVAALGSPGAPALSLRGEPLTI 60

DB 2 GSLSRRKLT-SSPSPSSSGPDQEPVSWQPRHRKVAVALGSPGAPALSLRGEPLTI 60

QY 61 VSEDGDMWTVLSEVSGREYNIPSVHAKVSHGLYEGSRKAEELLPLGNPGAPFLIR 120

DB 61 ISEDDGDMWTVLSEVSGREYNIPSVHAKVSHGLYEGSRKAEELLPLGNPGAPFLIR 120

QY 121 ESOTRRGYSYLSVRLSPASMDRIHRIHCLDGMWLYISPRITFPSIQALVDHYS- 180

DB 121 ESOTRRGYSYLSVRLSPASMDRIHRIHCLDGMWLYISPRITFPSIQALVDHYS- 180

QY 181 DICCLKEPCVLQRAAGPLPGDIPLPVTVQRTPLNWKELDSLLFSEA-ATGEESILSEG 239

DB 181 GICCPLEPCVLQKGLPGDTPPTVTVPTSSLMWKLDSLLFLEAPASGASALLSEG 240

QY 240 LRESLSYSISLAED--PLDDA 260

DB 241 LRESLSYSISLAED--PLDDA 259

RESULT 5

Q08WY18 PRELIMINARY; PRT; 210 AA.

AC Q08WY18; 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

OS Modulator of antigen receptor signaling, putative splice isoform

OC MARS-V.

OC Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OK NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Loreto M.P., McGlade C.J.,

RT "Modulator of Antigen Receptor Signaling (MARS) - putative splice

RT variant."

RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL; AR290986; AAL38198.1; -

DR InterPro; IPR000980; SH2.

DR InterPro; IPR001452; SH3.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3; 1.

DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00452; SH3DOMAIN.

DR ProDom; PD000093; SH2; 1.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 1.

DR PROSITE; PS50001; SH2; 1.

DR PROSITE; PS50002; SH3; 1.

KW Receptor.

SQ SEQUENCE 210 AA; 23103 MW; BBD62208E53A472E CRC64;

Query Match 69.4%; Score 933.5; DB 4; Length 210;

Best Local Similarity 89.3%; Pred. No. 2e-77;

Matches 184; Conservative 3; Mismatches 12; Indels 7; Gaps 1;

QY 1 GSLPSRRKSLPSPLSSVQGGPYTMEARSKATVAALGSPGAPALSLRGEPLTI 60

DB 2 GSLSRRKLT-SSPSPSSSGPDQEPVSWQPRHRKVAVALGSPGAPALSLRGEPLTI 61

QY 61 VSEDGDMWTVLSEVSGREYNIPSVHAKVSHGLYEGSRKAEELLPLGNPGAPFLIR 120

DB 62 VSEDGDMWTVLSEVSGREYNIPSVHAKVSHGLYEGSRKAEELLPLGNPGAPFLIR 121

QY 121 ESOTRRGYSYLSVRLSPASMDRIHRIHCLDGMWLYISPRITFPSIQALVDHYS- 177

DB 122 ESOTRRGYSYLSVRLSPASMDRIHRIHCLDGMWLYISPRITFPSIQALVDHYS- 181

QY 178 ----LADICCLKEPCVLQRAAGPL 199

DB 182 APWQGYTPCCACEDTQLERAGQLP 207

RESULT 6

Q09D129 PRELIMINARY; PRT; 179 AA.

AC Q09D129; 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

OS A93000982IRIK protein.

OC Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OK NCBI_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=RETINA.

RA MEDLINE=1085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,

RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochwa H.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Guenrich S., Hall D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohatsu S.,

RA Hayashizaki Y.;

RT Functional annotation of a full-length mouse cDNA collection.",
 RL Nucleotide accession numbers: AF001200.
 DR EMBL: AK020837; BAB32223.1; -
 DR HSSP: P06239; 1LKK.
 DR MGD: MGI:1925049; A930009E2RLrk.
 DR InterPro: IPR000980; SH2.
 DR Pfam: PF00017; SH2, 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR ProDom: PD000093; SH2, 1.
 DR SMART: SMO0252; SH2; 1.
 DR PROSITE: PS0001; SH2; 1.
 SQ SEQUENCE 179 AA; 19926 MW; 60477AACF4003FCD CRC64;

Query Match	55.8%;	Score 751.5;	DB 11;	Length 179;
Best Local Similarity	82.3%;	Pred. No. 7.1e-61;		
Matches 149;	Conservative 11;	Mismatches 18;	Indels 3;	Gaps 2

[illegible]

RESULT 7			
ID	OBOLX8	PRELIMINARY;	PRT; 280 AA.
AC	OBOLX8		
AD	OBOLX8		
DT	01-JUN-2002 (TREMblrel. 21, Created)		
DT	01-JUN-2002 (TREMblrel. 21, Last sequence update)		
DT	01-JUN-2002 (TREMblrel. 21, Last annotation update)		
DE	Src-1-like adapter protein SHAP (Fragment).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
NCBI_Taxid=10090;			
LN	[1]		

RP SEQUENCE FROM N.A.
RC STRAIN=IL5, AND ISS;
RX MEDLINE=21363810; PubMed=11471062;
RZ Ehringer M.A., Thompson J.J., Conroy O., Xu Y., Yang F., Canniff J.
R1 Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
R2 "High-throughput sequence identification of gene coding variants
R3 within alcohol-related OTLs.";
R4 Mamm. Genome 12:657-663(2001).
R5 [2]
RN SEQUENCE FROM N.A.
RP Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RC STRAIN=IL5, AND ISS;
RZ Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
R1 Submitted (FEB-2002) to the EMBL/Genbank/DBS databases.
R2 EMBL, AY079449; MML87537.1; -
R3 EMBL, AY079450; MML87536.1; -
R4 NON_TER 1
R5 FT 280
R6 SEQUENCE 280 AA; 31549 MW; A05C33BF7FEAD951 CRC64;

Query Match 36.8%; Score 495.5; DB 11; Length 280;
Best Local Similarity 43.9%; Pred. No. 3.4e-37;
Matches 116; Conservative 38; Mismatches 81; Indels 29; Gaps 7;

0Y 8 KSLBPS---LSSVGGGPPVMEARSKATAVALGSPAGCPAELSLRLCPPLTIVSED 64
|| | ||| | | | : | | | : : :
|| | ||| | | | : | | | : : :

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Db      5  KATSPSPSRPLSS-----EGLSDFLAV-LTDVPSDIPPIFRGEXLNVISDE  54

Qy      65  GMMWTVLSEVSGENNIIEBIVAAKYSIGWLYEELSEKAEELLLPBNPGCAFLLRESQT  124
Db      55  GGMWVAISLSTGSESYIPICIVARYGWLFEGLGRDAEELLQLPPTKIGSFMRESST  114

Qy      125  RGGSYSLSVRLSRPASMDIRHYRIHCLDNGMLYISPRLTFPELQALVDHYSGLDDIC  184
Db      115  KKGFLYSLSVR-----HRQVKKHYRIPLPNWVYIISPRLTFQGLDLYVHYSEVADGLCC  166

Qy      185  LIKEPCVQLQR-----AGPLPGKDIPLVYVYQRPPLNKKLELDSLLSFEAATG-----EESL  233
Db      169  VITTECLANQIIPAPTHSPSPCTSPGSFVTLROKTPDKMRVRSRQSGEGENPNPLRVDEST  228

Qy      236  LSEGRLRESLSFYSL-NDKVAVSLD  258
Db      229  PFIYGRBSIASYLSLTCDDSSSFD  252

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Db 229 PSYGLRESIASYLSLTGDDSSSF 252

ID	Accession	Species	Gene	Protein	Length	Score	E-value	Annotations
OC60898	PRELIMINARY			PRT	281 AA			
AC	OC60898							
DT	01-NOV-1996	(TrEMBLrel. 01, Created)						
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)						
DT	01-MAR-2002	(TrEMBLrel. 20, Last annotation update)						
DE	SRC-1-like adapter protein.							
GN	SRC-1 OR SLAP.							
OS	Mus musculus (mouse)							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus							
OX	NCBI_TaxID=10090;							

RX MEDLINE=95370243; PubMed=7543899;
RA Pandey A., Dhan H., Dixit V.M.;
RT "Characterization of a novel Src-like adapter protein that associates
RT with the Eck receptor tyrosine kinase.";
RL J. Biol. Chem. 270:19201-19204(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20093965; PubMed=10630289;
RA Carrier A., Nguyen C., Vitorero G., Granjeaud S., Rocha D.,
RA Bernard K., Mazek A., Ferrier P., Malissen M., Naquet P.,
RA Malissen B., Jordan B.;
RT "Differential gene expression in CD3e- and Rag1-deficient thymuses:
RT definition of a set of genes potentially involved in thymocyte

RT maturation.";
 RL Immunogenetics 50:255-270(1999).
 CC -I- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC EMBL: U29056; AAA82756.1. "-."
 DR EMBL: AJ131777; CAB66139.1; "-."
 DR HSSP: P16277; 1BLK
 DR MGD: MGI:104295; S1a.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00017; SH2, 1.
 DR Pfam: PF00018; SH3, 1.
 DR PRINTS: PRO0401; SH2DOMAIN.
 DR ProDom: PD000093; SH2, 1.
 DR SMART: SM00252; SH2, 1.
 DR SMART: SM00326; SH3, 1.
 DR PROSITE: PSS0001; SH2, 1.
 DR PROSITE: PSS0002; SH3, 1.
 DR SH3 domain.
 KW SEQUENCE 281 AA; 31680 MW; B347921656A74DA1 CRC64;

Query Match	36.8%;	Score 495.5;	DB 11;	Length 281;
Best Local Similarity	43.9%;	Pred. No. 3.5e-37;		
Matches 116; Conservative	38;	Mismatches 81;	Indels 29;	Gaps 7;

QY 8 KSLPSPS---ISSSVQGQGPVTMEERSKATAVALGSPACGPAELSLRCEPLTIVSED 64
|| ||| | | : | | | : :
|| ||| | | : | | | : :

Db 6_KSTPSPSERPLSS-----EGLESDPLAV-LTDVPSDIPSPILFRRGKRLRVISDE 55
 Qy 65 GDMWTLSEVSGREYNIPSVHAKVSHGMLYEGSLREKAEELLILPGNPGAFILRSQ 124
 Db 56 GWMWKAISLSTGRESYIPGICVAVYHGMVFEGLGRDCAEELLQQLDPTIGSFMRES 115
 Qy 125 RRGYSVLSVRLSRPAMDRIRHYRICHLDNGMLYISPLTFPSLOALVDHYSELDADICC 184
 Db 116 KKGFSLSVSR-----HRQVHYRIFRLPNMNYISPLTFQCLDLDVHYSEVADGLCC 169
 Qy 185 LKKEPCVLOR-----AGPLPKDIPLPVTVQRTPLNWKELDSLLFSEATG---EESL 235
 Db 170 VLTPLAQNIPAPTSHPSPCTSPGSPVTLRKQTDWKRVRSLQEGSEGAENPLRVESL 229
 Qy 236 LSEGLRESLSFYISL-NDKAVSLD 258
 Db 230 FSYGLRESIASYLSLTGDDSSSP 253

RESULT 9
 ID Q13239 PRELIMINARY; PRT; 276 AA.
 AC Q13239;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Putative SRC-like adapter protein (SLAP) (SRC-like-adapter).
 GN SLAP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96423054; Pubmed=8825655;
 RA Angrist M., Wells D.E., Chakravarti A., Pandey A.;
 RT "Chromosomal localization of the mouse Src-like adapter protein (Slap)
 RT gene and its putative human homolog SLA.";
 RL Genomics 30:623-625(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RA Meijerink P.H.S., Zorn G., Bikker H., Bolhuis P.A., Baas F.;
 RL Submitted (Feb-1997) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Ohtsuki T., Hatake K., Ikeda M., Tomizuka H., Terui Y., Uwai M.,
 RA Mura Y.;
 RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Blechschmidt K., Kalaydjieva L., Goodman R., Gresham D., Baas F.,
 RA Jonge, Rd, Schilhabel M., Wen G., Menzel U., Detle M., Baugart C.,
 RA Rosenthal A.;
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BONE MARROW;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; U30473; AAC50357.1; -
 DR EMBL; U44403; AAC27662.1; -
 DR EMBL; D89077; BA13758.1; -
 DR EMBL; AF305872; AAG17933.1; -
 DR EMBL; BC007042; AAH07042.1; -
 DR HSSP; P08631; 3HCK.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR ProDom; PD000093; SH2; 1.

DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR SH3 domain.
 SQ SEQUENCE 276 AA; 31156 MW; B0FC07B2ECA378 CRC64;
 Query Match 36.1%; Score 485.5; DB 4; Length 276;
 Best Local Similarity 40.7%; Pred. No. 2,8e-36;
 Matches 103; Conservative 43; Mismatches 84; Indels 23; Gaps 4;
 Qy 8 KSLPSPSSSSVOCGPVTMEARSKATAVAGLFFPAGPAELSLRGLPPTIVSEDCGM 67
 Db 6 KSTPAPA-----ERLPNPEGLDSDPLAVLSDYSPSPDISPIPRRGKRLRVISDEGM 58
 Qy 68 WTLSEVSGREYNIPSVHAKVSHGMLYEGSLREKAEELLILPGNPGAFILRSQ 127
 Db 59 WKAISLSTGRESYIPGICVAVYHGMVFEGLGRDCAEELLQQLDPTIGSFMRES 118
 Qy 128 SYSLSVRLSRPAMDRIRHYRICHLDNGMLYISPLTFPSLOALVDHYSELDADICCL 187
 Db 119 FYLSVSR-----HRQVHYRIFRLPNMNYISPLTFQCLDLDVHYSEVADGLCCVLT 172
 Qy 188 EPOVQGRAPLPGDIPLPVTVQRTPLNWKELDSLLFSEATG-----EESLSEGL 240
 Db 173 TPCLTSTAPAVPAVSSPVLTKQTVDMRVSR--LQDEPGEPLGVDESLSYGL 229
 Qy 241 RESLSFYISLND 253
 Db 230 RESIASYLSLTSE 242

RESULT 10
 ID Q9DDK6 PRELIMINARY; PRT; 502 AA.
 AC Q9DDK6;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Src-family tyrosine kinase SKC.
 GN Salmosalar (Atlantic salmon).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OK NCBI_TaxID=8030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hordvik I., Male R.;
 RA "A leukocyte cDNA of Atlantic salmon encoding a Src-family tyrosine
 RT kinase.";
 RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; AF321110; AAG38611.1; -
 DR HSSP; P08631; 1AD5.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Set_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; Tyr_pkinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TYKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KM ATP-binding; Kinase; SH3 domain; Transferase.
 SQ SEQUENCE 502 AA; 5660 MW; 82DF0D677AA99980 CRC64;

Query Match 27.5%; Score 370.5; DB 13; Length 502;
 Best Local Similarity 42.4%; Pred. No. 2,1e-25;
 Matches 81; Conservative 29; Mismatches 66; Indels 15; Gaps 3;

QY 14 SLSSVGGQGPVTMEARSKATAVALGSPAGAPALSLRLGEPPLTVSEDDGMWTVLSE 73
 DB 45 STGSPSPDGP-----ESTALALVDYEGINEGDLGPKKDKKTLQSGEMRAQSI 96
 QY 74 VSGREYNIPSVHAKVS---HGMLYEGLSREKAEELLIPNPGCAFILRESQTRRGYS 130
 DB 97 STGDEGFIPSNYVALDLSLETETEMFPGVSRDAERQLLASGNKGSFMIDSETTKGSYS 156
 QY 131 LSVRLSPASWDRIHRYRHICLDNGMLYISPLTPFSLQALVDHYSEIADICLLKEPC 190
 DB 157 LSVRSDSDSGDLYKHYKIRTLNDNGFIISPLITFTTLQELVSHYKKLGDLQALTPC 216
 QY 191 VLQRAPLPK 201
 DB 217 L-----SPKPK 223

RESULT 11

ID 013064 PRELIMINARY; PRT; 488 AA.

AC 013064;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Lys protein tyrosine kinase.
 GN LYN.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Fipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 CX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fukami Y., Funabiki K., Sato K.;
 RT "Nucleotide sequence of Xenopus Lys protein tyrosine kinase.";
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; AB003358; BAA20078.1; -;
 DR HSSP; P08631; IAD5.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KM ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 488 AA; 55794 MW; B7E7066B6BA92B2 CRC64;

Query Match 27.1%; Score 364.5; DB 13; Length 488;
 Best Local Similarity 40.1%; Pred. No. 7.1e-25;
 Matches 81; Conservative 33; Mismatches 69; Indels 19; Gaps 4;

QY 5 SRRKS-LPSPSSSSVGGQGPVTMEARSKATAVALGSPAGAPALSLRLGEPPLTVSE 63
 DB 22 SRTSLIPQKQKIQIDIEQNI-----VIALPYGHHEDLSFKKGEKLVLEE 71
 QY 64 DGMWTVLSEVSGREYNIPSVHAKV---SHGMLYEGLSREKAEELLIPNPGCAFIL 119
 DB 72 HGEWKKAKSLSTKKGFIPSNYVALVTLTETEMFFDQLTRKDAERQLLAPGNNGAFIL 131
 QY 120 RESQTRRGYSLSVRLSPASWDRIHRYRHICLDNGMLYISPLTPFSLQALVDHYSELA 179
 DB 132 RESFTSGSYSLSDIDCDPQGVIVHYKIRTLNDNGGVYISPLITFTTINEMIQHYQKA 191
 QY 180 DDLCLLKEPCVLQRAPLPK 201
 DB 192 DGLCRKLDKPCF---SPKPK 209

RESULT 12

ID 09HB17 PRELIMINARY; PRT; 161 AA.

AC 09HB17;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Src-like adapter protein (Fragrant).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Blechschmidt K., Kalaydjieva L., Goodman R., Gresham D., Baas F.,
 RA Jonke, Rd, Rosenthal M.B., Menzel U., Dettle M.D., Baumgart C.,
 RA Jahn N., Rosenthal A.;
 RT "Chromosome 8 genomic sequence";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; AF23100; AAG29878.1; -;
 DR HSSP; P08631; 3HCK.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KM SH3 domain.
 KW NON TER 161
 FT
 SQ SEQUENCE 161 AA; 18493 MW; FC2854668045B20 CRC64;

Query Match 26.9%; Score 362.5; DB 4; Length 161;
 Best Local Similarity 44.4%; Pred. No. 2.4e-25;
 Matches 75; Conservative 27; Mismatches 54; Indels 13; Gaps 2;

QY 8 KSLPSLSSVGGQGPVTMEARSKATAVALGSPAGAPALSLRLGEPPLTVSEDDW 67
 DB 6 KSTPAPA-----ERFLPNPEGUDDFLAVLSDVPSDIPPIFRKGEKLVISDEGW 58
 QY 68 WTVLSEVSGREYNIPSVHAKVSHGMLYEGLSREKAEELLIPNPGCAFILRESQTRRG 127
 DB 59 WKALSLSTGRSEYIPIQVAVHYHGMFLBGLGRDAEELLQLPPTKVGSMIRSETKKG 118

Qy 126 SYSISVRLSRPASMDRIRHRIHCLDNGMLYISPRLTSPSIALVDHYS 176
 DB 119 FYSLSVR-----HROVGHRIIFPLPNMNYISPRLTSCLEDLVNHS 161

RESULT 13

Q96IN1 PRELIMINARY; PRT; 505 AA.
 AC Q96IN1
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NC NCI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strauberg R.;
 RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC007371; AA07371.1;
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProSite; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
 DR ProSite; PS50011; PROTEIN_KINASE_DOM; 1.
 DR ProSite; PS50001; SH2; 1.
 DR ProSite; PS50002; SH3; 1.
 KW ATP-binding; Transferase.
 SQ SEQUENCE 505 AA; 57706 MW; B5F73BEF839176 CRC64;

Query Match 26.5%; Score 356.5; DB 4; Length 505;
 Best Local Similarity 44.2%; Pred. No. 4e-24; Matches 76; Conservative 24; Mismatches 67; Indels 5; Gaps 2;

Qy 24 PVTMEARSRKATVAVALGSPAGPAELSLRLGEPLTIVSEDDGWTVLSEVSGREYNIPS 83
 DB 51 PRDEHLEDKHFVALDYDTAMNDRLQMLKSGKQLQVKGKGTGWTLARSLVTGRGYVPS 110
 Qy 84 VHVAKVS---HGWLVEGLSRKAEELLIPGPGAFILRESQTRGSGYSLSRPA 139
 DB 111 NFAKVSLEMERKFFRSGQKKEKRLQPLPKKAGSFLRESSTNGASLSVR-DVTT 169
 Qy 140 SMDRIHRYRIHCLDNGMLYISPRLTSPSIALVDHYSLEADICLLKPCV 191
 DB 170 QGELIKHYKIRCLDEGGYVISPRTFPSIQALVQHSKKGDLQRLTLPCV 221

RESULT 14

Q95M32 PRELIMINARY; PRT; 509 AA.
 AC Q95M32
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 OS Lck protein.
 GN LCK.
 OC Hylobates sp. (gibbon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 NC NCI_TaxID=9581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Picard C.;

RL Thesis (2001). Department of Experimental Oncology Laboratory, U.
 DR EMBL; AJ320182; CAC44027.1; --
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProSite; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
 DR ProSite; PS50011; PROTEIN_KINASE_DOM; 1.
 DR ProSite; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
 DR ProSite; PS50001; SH2; 1.
 DR ProSite; PS50002; SH3; 1.
 KW ATP-binding; Transferase.
 SQ SEQUENCE 509 AA; 57946 MW; F1BF5C237C8D57E CRC64;

Query Match 25.6%; Score 344; DB 6; Length 509;
 Best Local Similarity 41.1%; Pred. No. 5.6e-23; Matches 74; Conservative 26; Mismatches 70; Indels 10; Gaps 2;

Qy 25 VTMERSRKAT-----AVLGSFPAGPAELSLRLGEPLTIVSEDDGWTVLSEVSGRE 78
 DB 49 VTGEGSNPPASPLQDNLVIALHSYEPHSDGDLGEKKEQRLILESGEMWAGSLTTGQE 108
 Qy 79 YNPSVHVAKVS---HGWLVEGLSRKAEELLIPGPGAFILRESQTRGSGYSLSVR 134
 DB 109 GFIPFVFAKVSLEPEPWFKNLSKDAERQLAPGNTGSPFLRESSTNGASLSVR 168
 Qy 135 LSRRPASMDRIRHRIHCLDNGMLYISPRLTSPSIALVDHYSLEADICLLKPCV 194
 DB 169 DFDQNGEVAKYKIRLNDGGFYISPRTFGHLVRYTNASDGLCTRLSPCQYK 228

RESULT 15

Q91X65 PRELIMINARY; PRT; 509 AA.
 AC Q91X65
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DT Similar to lymphocyte-specific protein tyrosine kinase.
 GN LCK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 NC NCI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SALIVARY GLAND;
 RA Strauberg R.;
 RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC011474; AAH11474.1; --
 DR MGD; MGI:96756; lck.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProSite; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
 DR ProSite; PS50011; PROTEIN_KINASE_DOM; 1.
 DR ProSite; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
 DR ProSite; PS50001; SH2; 1.
 DR ProSite; PS50002; SH3; 1.
 KW ATP-binding; Kinase; Transferase.

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SQ SEQUENCE 509 AA; 57942 MW; 3513102F49A7FD0B CRC64;

Query Match

25.4%; Score 342.5; DB 11; Length 509;
20.6%; No. 7 79-33.

Best Local Similarity 39.6%; Pred. No. 7, 7e-23;
Matches 78; Conservative 28; Mismatches 84; Indels 7; Gaps 2;

Matches 71

Matches 71

Matches 71

Matches 71

Matches 71

Qy 2 SLSRRKRLPPSLSSVGGQGPVMEERKSKTAAVAGSPAGGAPMELSLRKGPELTV 61
 |||||
 Db 35 SLPIRNGSEVNDPL---VYTESLPPASPLQDNLVYALHSTPEPHSDGLFEKSGQLRIL 91
 |||||
 Qy 62 SEDGDMMTVLSEVSGREYNIPSVHAVAKV---HGWLVEGLSRKEAELELLPGNPGGAF 117
 :|||:
 Db 92 EGGEGEMVAQSLTGGQGFIPNFVAAKANSLEDEPFKNLSRDAERQLLPGNTHGSF 151
 |||||
 Qy 118 LIRRESQTRRGYSLSVAVLSRPASMRIRHRIICLDNGMLYSRLLFFPSLQALVDHISE 177
 |||||
 Db 152 LIRRESSTAGSFSLSVAVDDQNGEVAHVKYKINLNDGGGFYSIRITFFGLDHLVRYHTN 211
 |||||
 Qy 178 LADDIICLLKEPCVLQR 194
 :|||:
 Db 212 ASDGLCTKLSRFCQYCK 228

Qy 2 SLSRRKRLPPSLSSVGGQGPVMEERKSKTAAVAGSPAGGAPMELSLRKGPELTV 61
 |||||
 Db 35 SLPIRNGSEVNDPL---VYTESLPPASPLQDNLVYALHSTPEPHSDGLFEKSGQLRIL 91
 |||||
 Qy 62 SEDGDMMTVLSEVSGREYNIPSVHAVAKV---HGWLVEGLSRKEAELELLPGNPGGAF 117
 :|||:
 Db 92 EGGEGEMVAQSLTGGQGFIPNFVAAKANSLEDEPFKNLSRDAERQLLPGNTHGSF 151
 |||||
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 Qy 178 LADDIICLLKEPCVLQR 194
 :|||:
 Db 212 ASDGLCTKLSRFCQYCK 228

Qy 2 SLSRRKRLPPSLSSVGGQGPVMEERKSKTAAVAGSPAGGAPMELSLRKGPELTV 61
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